



REVSecond Substitute Sequence Listing 1829-4004US1.TXT
SUBSTITUTE SEQUENCE LISTING

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<141> 2002-01-07

<150> 60/260,080

<151> 2001-01-06

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<170> PatentIn Ver. 2.1

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gctgagcctc	ctataatttac	aatgtctata	gggactgttt	tactgcctgt	gtattttctg	4920
ctagagagtt	agcaatgtta	gagctagaac	agattagaat	ttctaaacag	tatcatgcac	4980
agttgggtgtg	agtgatcagt	gtgcattgta	tggcatgcat	ggttgtgaat	tattctctgt	5040
tctccaaata	ctgtttcttt	aactcagata	ttttgttag	tgcttaggcc	acttcattta	5100
tttttcgtca	tggtacttta	ctgacttctc	tttattcaat	tctccacgcc	ctcaccacaaa	5160
aaaactgtct	caaaatgaga	atatttttat	tcttcatggg	gagtctagaa	aacgccccac	5220
ttcatttctga	ttaaaaaatt	cttccatggt	tttaaatatc	agaaccagac	ctttcttact	5280
gtgtatctta	gcccatttgt	gtctctataa	caacaaccag	ctttcaaagg	aactaataga	5340
gtgaaaactc	actcattacc	acgaggatgg	cacaagcgat	tcacgtagga	tctgcccctg	5400
tgaccacaaac	acctcccat	gggccccact	tccaacactg	gtgatcacat	ttcaacatga	5460
ggtttaggga	aacaaatgcc	taaactacag	cactgtacat	aaactaacag	gaaatgctgc	5520
ttttgatcct	caaagaagtg	atatagccaa	aattgttaatt	taagaagcct	ttgtcagtat	5580
agcaagatgt	taactataga	atcaatctag	gagtattcac	tgtaaaattc	aactttttctg	5640
tatgtttgaa	cattttcaca	atctcatagg	agtttttaaa	aagaagagaa	agaagatata	5700
cttgctttg	gagaaatcta	ctttttgact	tacatgggtt	tgctgtaatt	aagtgcccaa	5760
tattgaaaagg	ctgcaagtac	tttghtaatca	ctctttggca	tgggtaaata	agcatggtaa	5820
cttatattga	aatatagtc	tcttgctttg	gataactgta	aagggaacca	tgctgataga	5880
ctggaaatag	aagtaaatgt	gtttattgaa	aaaaaaaaa	aaaa		5924

<210> 3

<211> 1332

<212> PRT

<213> Homo sapiens

<400> 3

Met Arg Asn Leu Lys Leu Phe Arg Thr Leu Glu Phe Arg Asp Ile Gln
1 5 10 15

Gly Pro Gly Asn Pro Gln Cys Phe Ser Leu Arg Thr Glu Gln Gly Thr
20 25 30

Val Leu Ile Gly Ser Glu His Gly Leu Ile Glu Val Asp Pro Val Ser
35 40 45

Arg Glu Val Lys Asn Glu Val Ser Leu Val Ala Glu Gly Phe Leu Pro

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

50

55

60

Glu Asp Gly Ser Gly Arg Ile Val Gly Val Gln Asp Leu Leu Asp Gln
65 70 75 80
Glu Ser Val Cys Val Ala Thr Ala Ser Gly Asp Val Ile Leu Cys Ser
85 90 95
Leu Ser Thr Gln Gln Leu Glu Cys Val Gly Ser Val Ala Ser Gly Ile
100 105 110
Ser Val Met Ser Trp Ser Pro Asp Gln Glu Leu Val Leu Leu Ala Thr
115 120 125
Gly Gln Gln Thr Leu Ile Met Met Thr Lys Asp Phe Glu Pro Ile Leu
130 135 140
Glu Gln Gln Ile His Gln Asp Asp Phe Gly Glu Ser Lys Phe Ile Thr
145 150 155 160
Val Gly Trp Gly Arg Lys Glu Thr Gln Phe His Gly Ser Glu Gly Arg
165 170 175
Gln Ala Ala Phe Gln Met Gln Met His Glu Ser Ala Leu Pro Trp Asp
180 185 190
Asp His Arg Pro Gln Val Thr Trp Arg Gly Asp Gly Gln Phe Phe Ala
195 200 205
Val Ser Val Val Cys Pro Glu Thr Gly Ala Arg Lys Val Arg Val Trp
210 215 220
Asn Arg Glu Phe Ala Leu Gln Ser Thr Ser Glu Pro Val Ala Gly Leu
225 230 235 240
Gly Pro Ala Leu Ala Trp Lys Pro Ser Gly Ser Leu Ile Ala Ser Thr
245 250 255
Gln Asp Lys Pro Asn Gln Gln Asp Ile Val Phe Phe Glu Lys Asn Gly
260 265 270
Leu Leu His Gly His Phe Thr Leu Pro Phe Leu Lys Asp Glu Val Lys
275 280 285
Val Asn Asp Leu Leu Trp Asn Ala Asp Ser Ser Val Leu Ala Val Arg
290 295 300
Leu Glu Asp Leu Gln Arg Glu Lys Ser Ser Ile Pro Lys Thr Cys Val
305 310 315 320
Gln Leu Trp Thr Val Gly Asn Tyr His Trp Tyr Leu Lys Gln Ser Leu
325 330 335
Ser Phe Ser Thr Cys Gly Lys Ser Lys Ile Val Ser Leu Met Trp Asp
340 345 350
Pro Val Thr Pro Tyr Arg Leu His Val Leu Cys Gln Gly Trp His Tyr
355 360 365
Leu Ala Tyr Asp Trp His Trp Thr Thr Asp Arg Ser Val Gly Asp Asn
370 375 380
Ser Ser Asp Leu Ser Asn Val Ala Val Ile Asp Gly Asn Arg Val Leu

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

385 390 395 400
 Val Thr Val Phe Arg Gln Thr Val Val Pro Pro Pro Met Cys Thr Tyr
 405 410 415
 Gln Leu Leu Phe Pro His Pro Val Asn Gln Val Thr Phe Leu Ala His
 420 425 430
 Pro Gln Lys Ser Asn Asp Leu Ala Val Leu Asp Ala Ser Asn Gln Ile
 435 440 445
 Ser Val Tyr Lys Cys Gly Asp Cys Pro Ser Ala Asp Pro Thr Val Lys
 450 455 460
 Leu Gly Ala Val Gly Gly Ser Gly Phe Lys Val Cys Leu Arg Thr Pro
 465 470 475 480
 His Leu Glu Lys Arg Tyr Lys Ile Gln Phe Glu Asn Asn Glu Asp Gln
 485 490 495
 Asp Val Asn Pro Leu Lys Leu Gly Leu Leu Thr Trp Ile Glu Glu Asp
 500 505 510
 Val Phe Leu Ala Val Ser His Ser Glu Phe Ser Pro Arg Ser Val Ile
 515 520 525
 His His Leu Thr Ala Ala Ser Ser Glu Met Asp Glu Glu His Gly Gln
 530 535 540
 Leu Asn Val Ser Ser Ser Ala Ala Val Asp Gly Val Ile Ile Ser Leu
 545 550 555 560
 Cys Cys Asn Ser Lys Thr Lys Ser Val Val Leu Gln Leu Ala Asp Gly
 565 570 575
 Gln Ile Phe Lys Tyr Leu Trp Glu Ser Pro Ser Leu Ala Ile Lys Pro
 580 585 590
 Trp Lys Asn Ser Gly Gly Phe Pro Val Arg Phe Pro Tyr Pro Cys Thr
 595 600 605
 Gln Thr Glu Leu Ala Met Ile Gly Glu Glu Glu Cys Val Leu Gly Leu
 610 615 620
 Thr Asp Arg Cys Arg Phe Phe Ile Asn Asp Ile Glu Val Ala Ser Asn
 625 630 635 640
 Ile Thr Ser Phe Ala Val Tyr Asp Glu Phe Leu Leu Leu Thr Thr His
 645 650 655
 Ser His Thr Cys Gln Cys Phe Cys Leu Arg Asp Ala Ser Phe Lys Thr
 660 665 670
 Leu Gln Ala Gly Leu Ser Ser Asn His Val Ser His Gly Glu Val Leu
 675 680 685
 Arg Lys Val Glu Arg Gly Ser Arg Ile Val Thr Val Val Pro Gln Asp
 690 695 700
 Thr Lys Leu Val Leu Gln Met Pro Arg Gly Asn Leu Glu Val Val His
 705 710 715 720

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

His Arg Ala Leu Val Leu Ala Gln Ile Arg Lys Trp Leu Asp Lys Leu
725 730 735

Met Phe Lys Glu Ala Phe Glu Cys Met Arg Lys Leu Arg Ile Asn Leu
740 745 750

Asn Pro Ile Tyr Asp His Asn Pro Lys Val Phe Leu Gly Asn Val Glu
755 760 765

Thr Phe Ile Lys Gln Ile Asp Ser Val Asn His Ile Asn Leu Phe Phe
770 775 780

Thr Glu Leu Lys Glu Glu Asp Val Thr Lys Thr Met Tyr Pro Ala Pro
785 790 795 800

Val Thr Ser Ser Val Tyr Leu Ser Arg Asp Pro Asp Gly Asn Lys Ile
805 810 815

Asp Leu Val Cys Asp Ala Met Arg Ala Val Met Glu Ser Ile Asn Pro
820 825 830

His Lys Tyr Cys Leu Ser Ile Leu Thr Ser His Val Lys Lys Thr Thr
835 840 845

Pro Glu Leu Glu Ile Val Leu Gln Lys Val His Glu Leu Gln Gly Asn
850 855 860

Ala Pro Ser Asp Pro Asp Ala Val Ser Ala Glu Glu Ala Leu Lys Tyr
865 870 875 880

Leu Leu His Leu Val Asp Val Asn Glu Leu Tyr Asp His Ser Leu Gly
885 890 895

Thr Tyr Asp Phe Asp Leu Val Leu Met Val Ala Glu Lys Ser Gln Lys
900 905 910

Asp Pro Lys Glu Tyr Leu Pro Phe Leu Asn Thr Leu Lys Lys Met Glu
915 920 925

Thr Asn Tyr Gln Arg Phe Thr Ile Asp Lys Tyr Leu Lys Arg Tyr Glu
930 935 940

Lys Ala Ile Gly His Leu Ser Lys Cys Gly Pro Glu Tyr Phe Pro Glu
945 950 955 960

Cys Leu Asn Leu Ile Lys Asp Lys Asn Leu Tyr Asn Glu Ala Leu Lys
965 970 975

Leu Tyr Ser Pro Ser Ser Gln Gln Tyr Gln Asp Ile Ser Ile Ala Tyr
980 985 990

Gly Glu His Leu Met Gln Glu His Met Tyr Glu Pro Ala Gly Leu Met
995 1000 1005

Phe Ala Arg Cys Gly Ala His Glu Lys Ala Leu Ser Ala Phe Leu Thr
1010 1015 1020

Cys Gly Asn Trp Lys Gln Ala Leu Cys Val Ala Ala Gln Leu Asn Phe
1025 1030 1035 1040

Thr Lys Asp Gln Leu Val Gly Leu Gly Arg Thr Leu Ala Gly Lys Leu
1045 1050 1055

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Val Glu Gln Arg Lys His Ile Asp Ala Ala Met Val Leu Glu Glu Ser
1060 1065 1070
Ala Gln Asp Tyr Glu Glu Ala Val Leu Leu Leu Leu Glu Gly Ala Ala
1075 1080 1085
Trp Glu Glu Ala Leu Arg Leu Val Tyr Lys Tyr Asn Arg Leu Asp Ile
1090 1095 1100
Ile Glu Thr Asn Val Lys Pro Ser Ile Leu Glu Ala Gln Lys Asn Tyr
1105 1110 1115 1120
Met Ala Phe Leu Asp Ser Gln Thr Ala Thr Phe Ser Arg His Lys Lys
1125 1130 1135
Arg Leu Leu Val Val Arg Glu Leu Lys Glu Gln Ala Gln Gln Ala Gly
1140 1145 1150
Leu Asp Asp Glu Val Pro His Gly Gln Glu Ser Asp Leu Phe Ser Glu
1155 1160 1165
Thr Ser Ser Val Val Ser Gly Ser Glu Met Ser Gly Lys Tyr Ser His
1170 1175 1180
Ser Asn Ser Arg Ile Ser Ala Arg Ser Ser Lys Asn Arg Arg Lys Ala
1185 1190 1195 1200
Glu Arg Lys Lys His Ser Leu Lys Glu Gly Ser Pro Leu Glu Asp Leu
1205 1210 1215
Ala Leu Leu Glu Ala Leu Ser Glu Val Val Gln Asn Thr Glu Asn Leu
1220 1225 1230
Lys Asp Glu Val Tyr His Ile Leu Lys Val Leu Phe Leu Phe Glu Phe
1235 1240 1245
Asp Glu Gln Gly Arg Glu Leu Gln Lys Ala Phe Glu Asp Thr Leu Gln
1250 1255 1260
Leu Met Glu Arg Ser Leu Pro Glu Ile Trp Thr Leu Thr Tyr Gln Gln
1265 1270 1275 1280
Asn Ser Ala Thr Pro Val Leu Gly Pro Asn Ser Thr Ala Asn Ser Ile
1285 1290 1295
Met Ala Ser Tyr Gln Gln Gln Lys Thr Ser Val Pro Val Leu Asp Ala
1300 1305 1310
Glu Leu Phe Ile Pro Pro Lys Ile Asn Arg Arg Thr Gln Trp Lys Leu
1315 1320 1325
Ser Leu Leu Asp
1330

<210> 4

<211> 1332

<212> PRT

<213> Mus musculus

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

<400> 4

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Met Arg Asn Leu Lys Leu His Arg Thr Leu Glu Phe Arg Asp Ile Gln
 1      5      10      15
Ala Pro Gly Lys Pro Gln Cys Phe Cys Leu Arg Ala Glu Gln Gly Thr
      20      25      30
Val Leu Ile Gly Ser Glu Arg Gly Leu Thr Glu Val Asp Pro Val Arg
      35      40      45
Arg Glu Val Lys Thr Glu Ile Ser Leu Val Ala Glu Gly Phe Leu Pro
      50      55      60
Glu Asp Gly Ser Gly Cys Ile Val Gly Ile Gln Asp Leu Leu Asp Gln
      65      70      75      80
Glu Ser Val Cys Val Ala Thr Ala Ser Gly Asp Val Ile Val Cys Asn
      85      90      95
Leu Ser Thr Gln Gln Leu Glu Cys Val Gly Ser Val Ala Ser Gly Ile
      100      105      110
Ser Val Met Ser Trp Ser Pro Asp Gln Glu Leu Leu Leu Leu Ala Thr
      115      120      125
Ala Gln Gln Thr Leu Ile Met Met Thr Lys Asp Phe Glu Val Ile Ala
      130      135      140
Glu Glu Gln Ile His Gln Asp Asp Phe Gly Glu Gly Lys Phe Val Thr
      145      150      155      160
Val Gly Trp Gly Ser Lys Gln Thr Gln Phe His Gly Ser Glu Gly Arg
      165      170      175
Pro Thr Ala Phe Pro Val Gln Leu Pro Glu Asn Ala Leu Pro Trp Asp
      180      185      190
Asp Arg Arg Pro His Ile Thr Trp Arg Gly Asp Gly Gln Tyr Phe Ala
      195      200      205
Val Ser Val Val Cys Arg Gln Thr Glu Ala Arg Lys Ile Arg Val Trp
      210      215      220
Asn Arg Glu Phe Ala Leu Gln Ser Thr Ser Glu Ser Val Pro Gly Leu
      225      230      235      240
Gly Pro Ala Leu Ala Trp Lys Pro Ser Gly Ser Leu Ile Ala Ser Thr
      245      250      255
Gln Asp Lys Pro Asn Gln Gln Asp Val Val Phe Phe Glu Lys Asn Gly
      260      265      270
Leu Leu His Gly His Phe Thr Leu Pro Phe Leu Lys Asp Glu Val Lys
      275      280      285
Val Asn Asp Leu Leu Trp Asn Ala Asp Ser Ser Val Leu Ala Ile Trp
      290      295      300
Leu Glu Asp Leu Pro Lys Glu Asp Ser Ser Thr Leu Lys Ser Tyr Val
      305      310      315      320
Gln Leu Trp Thr Val Gly Asn Tyr His Trp Tyr Leu Lys Gln Ser Leu
      325      330      335

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REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Pro Phe Ser Thr Thr Gly Lys Asn Gln Ile Val Ser Leu Leu Trp Asp
340 345 350

Pro Val Thr Pro Cys Arg Leu His Val Leu Cys Thr Gly Trp Arg Tyr
355 360 365

Leu Cys Cys Asp Trp His Trp Thr Thr Asp Arg Ser Ser Gly Asn Ser
370 375 380

Ala Asn Asp Leu Ala Asn Val Ala Val Ile Asp Gly Asn Arg Val Leu
385 390 395 400

Val Thr Val Phe Arg Gln Thr Val Val Pro Pro Pro Met Cys Thr Tyr
405 410 415

Arg Leu Leu Ile Pro His Pro Val Asn Gln Val Ile Phe Ser Ala His
420 425 430

Leu Gly Asn Asp Leu Ala Val Leu Asp Ala Ser Asn Gln Ile Ser Val
435 440 445

Tyr Lys Cys Gly Asp Lys Pro Asn Met Asp Ser Thr Val Lys Leu Gly
450 455 460

Ala Val Gly Gly Asn Gly Phe Lys Val Pro Leu Thr Thr Pro His Leu
465 470 475 480

Glu Lys Arg Tyr Ser Ile Gln Phe Gly Asn Asn Glu Glu Glu Glu Glu
485 490 495

Glu Asp Phe Ala Leu Gln Leu Ser Phe Leu Thr Trp Val Glu Asp Asp
500 505 510

Thr Phe Leu Ala Ile Ser Tyr Ser His Ser Ser Ser Gln Ser Ile Ile
515 520 525

His His Leu Thr Val Thr His Ser Glu Val Asp Glu Glu Gln Gly Gln
530 535 540

Leu Asp Val Ser Ser Ser Val Thr Val Asp Gly Val Val Ile Gly Leu
545 550 555 560

Cys Cys Cys Ser Lys Thr Lys Ser Leu Ala Val Gln Leu Ala Asp Gly
565 570 575

Gln Val Leu Lys Ile Leu Trp Glu Ser Pro Ser Leu Ala Val Glu Pro
580 585 590

Trp Lys Asn Ser Glu Gly Ile Pro Val Arg Phe Val His Pro Cys Thr
595 600 605

Gln Met Glu Val Ala Thr Ile Gly Gly Glu Glu Cys Val Leu Gly Leu
610 615 620

Thr Asp Arg Cys Arg Phe Phe Ile Leu Val Thr Glu Val Ala Ser Asn
625 630 635 640

Ile Thr Ser Phe Ala Val Cys Asp Asp Phe Leu Leu Val Thr Thr His
645 650 655

Ser His Thr Cys Gln Gly Phe Ser Leu Ser Gly Ala Ser Leu Lys Met

670

685

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Gly Glu His Leu Met Gln Glu His Leu Tyr Glu Pro Ala Gly Leu Val
995 1000 1005

Phe Ala Arg Cys Gly Ala Gln Glu Lys Ala Leu Glu Ala Phe Leu Ala
1010 1015 1020

Cys Gly Ser Trp Gln Gln Ala Leu Cys Val Ala Ala Gln Leu Gln Met
1025 1030 1035 1040

Ser Lys Asp Lys Val Ala Gly Leu Ala Arg Thr Leu Ala Gly Lys Leu
1045 1050 1055

Val Glu Gln Arg Lys His Ser Glu Ala Ala Thr Val Leu Glu Gln Tyr
1060 1065 1070

Ala Gln Asp Tyr Glu Glu Ala Val Leu Leu Leu Leu Glu Gly Ser Ala
1075 1080 1085

Trp Glu Glu Ala Leu Arg Leu Val Tyr Lys Tyr Asp Arg Val Asp Ile
1090 1095 1100

Ile Glu Thr Ser Ile Lys Pro Ser Ile Leu Glu Ala Gln Lys Asn Tyr
1105 1110 1115 1120

Met Asp Phe Leu Asp Ser Glu Thr Ala Thr Phe Ile Arg His Lys Asn
1125 1130 1135

Arg Leu Gln Val Val Arg Ala Leu Arg Arg Gln Ala Pro Gln Val His
1140 1145 1150

Val Asp His Glu Val Ala His Gly Pro Glu Ser Asp Leu Phe Ser Glu
1155 1160 1165

Thr Ser Ser Ile Met Ser Gly Ser Glu Met Ser Gly Arg Tyr Ser His
1170 1175 1180

Ser Asn Ser Arg Ile Ser Ala Arg Ser Ser Lys Asn Arg Arg Lys Ala
1185 1190 1195 1200

Glu Arg Lys Lys His Ser Leu Lys Glu Gly Ser Pro Leu Glu Gly Leu
1205 1210 1215

Ala Leu Leu Glu Ala Leu Ser Glu Val Val Gln Ser Val Glu Lys Leu
1220 1225 1230

Lys Asp Glu Val Arg Ala Ile Leu Lys Val Leu Phe Leu Phe Glu Phe
1235 1240 1245

Glu Glu Gln Ala Lys Glu Leu Gln Arg Ala Phe Glu Ser Thr Leu Gln
1250 1255 1260

Leu Met Glu Arg Ala Val Pro Glu Ile Trp Thr Pro Ala Gly Gln Gln
1265 1270 1275 1280

Ser Ser Thr Thr Pro Val Leu Gly Pro Ser Ser Thr Ala Asn Ser Ile
1285 1290 1295

Thr Ala Ser Tyr Gln Gln Gln Lys Thr Cys Val Pro Ala Leu Asp Ala
1300 1305 1310

Gly Val Tyr Met Pro Pro Lys Met Asp Pro Arg Ser Gln Trp Lys Leu
1315 1320 1325

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Ser Leu Leu Glu
1330

<210> 5
<211> 1332
<212> PRT
<213> Homo sapiens

<400> 5
Met Arg Asn Leu Lys₅ Leu Phe Arg Thr Leu₁₀ Glu Phe Arg Asp Ile₁₅ Gln
Gly Pro Gly Asn₂₀ Pro Gln Cys Phe Ser₂₅ Leu Arg Thr Glu Gln₃₀ Gly Thr
Val Leu Ile₃₅ Gly Ser Glu His Gly₄₀ Leu Ile Glu Val Asp₄₅ Pro Val Ser
Arg Glu Val Lys Asn Glu Val₅₅ Ser Leu Val Ala Glu₆₀ Gly Phe Leu Pro
Glu Asp Gly Ser Gly Arg₇₀ Ile Val Gly Val Gln₇₅ Asp Leu Leu Asp Gln₈₀
Glu Ser Val Cys Val₈₅ Ala Thr Ala Ser Gly₉₀ Asp Val Ile Leu Cys Ser₉₅
Leu Ser Thr Gln Gln Leu Glu Cys Val₁₀₅ Gly Ser Val Ala Ser₁₁₀ Gly Ile
Ser Val Met₁₁₅ Ser Trp Ser Pro Asp₁₂₀ Gln Glu Leu Val Leu₁₂₅ Leu Ala Thr
Gly Gln Gln Thr Leu Ile Met₁₃₅ Met Thr Lys Asp Phe Glu Pro Ile Leu
Glu Gln Gln Ile His Gln₁₅₀ Asp Asp Phe Gly Glu₁₅₅ Ser Lys Phe Ile Thr₁₆₀
Val Gly Trp Gly Arg₁₆₅ Lys Glu Thr Gln Phe His Gly Ser Glu Gly₁₇₅ Arg
Gln Ala Ala Phe₁₈₀ Gln Met Gln Met His₁₈₅ Glu Ser Ala Leu Pro₁₉₀ Trp Asp
Asp His Arg₁₉₅ Pro Gln Val Thr Trp₂₀₀ Arg Gly Asp Gly Gln₂₀₅ Phe Phe Ala
Val Ser₂₁₀ Val Val Cys Pro Glu₂₁₅ Thr Gly Ala Arg Lys₂₂₀ Val Arg Val Trp
Asn Arg Glu Phe Ala Leu₂₃₀ Gln Ser Thr Ser Glu₂₃₅ Pro Val Ala Gly Leu₂₄₀
Gly Pro Ala Leu Ala₂₄₅ Trp Lys Pro Ser Gly₂₅₀ Ser Leu Ile Ala Ser₂₅₅ Thr
Gln Asp Lys Pro₂₆₀ Asn Gln Gln Asp Ile₂₆₅ Val Phe Phe Glu Lys₂₇₀ Asn Gly
Leu Leu His Gly His Phe Thr Leu Pro Phe Leu Lys Asp Glu Val Lys

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

275 Val Asn Asp Leu Leu Trp Asn Ala Asp Ser Ser Val Leu Ala Val Trp
 290 295 300
 Leu Glu Asp Leu Gln Arg Glu Glu Ser Ser Ile Pro Lys Thr Cys Val
 305 310 315 320
 Gln Leu Trp Thr Val Gly Asn Tyr His Trp Tyr Leu Lys Gln Ser Leu
 325 330 335
 Ser Phe Ser Thr Cys Gly Lys Ser Lys Ile Val Ser Leu Met Trp Asp
 340 345 350
 Pro Val Thr Pro Tyr Arg Leu His Val Leu Cys Gln Gly Trp His Tyr
 355 360 365
 Leu Ala Tyr Asp Trp His Trp Thr Thr Asp Arg Ser Val Gly Asp Asn
 370 375 380
 Ser Ser Asp Leu Ser Asn Val Ala Val Ile Asp Gly Asn Arg Val Leu
 385 390 395 400
 Val Thr Val Phe Arg Gln Thr Val Val Pro Pro Pro Met Cys Thr Tyr
 405 410 415
 Gln Leu Leu Phe Pro His Pro Val Asn Gln Val Thr Phe Leu Ala His
 420 425 430
 Pro Gln Lys Ser Asn Asp Leu Ala Val Leu Asp Ala Ser Asn Gln Ile
 435 440 445
 Ser Val Tyr Lys Cys Gly Asp Cys Pro Ser Ala Asp Pro Thr Val Lys
 450 455 460
 Leu Gly Ala Val Gly Gly Ser Gly Phe Lys Val Cys Leu Arg Thr Pro
 465 470 475 480
 His Leu Glu Lys Arg Tyr Lys Ile Gln Phe Glu Asn Asn Glu Asp Gln
 485 490 495
 Asp Val Asn Pro Leu Lys Leu Gly Leu Leu Thr Trp Ile Glu Glu Asp
 500 505 510
 Val Phe Leu Ala Val Ser His Ser Glu Phe Ser Pro Arg Ser Val Ile
 515 520 525
 His His Leu Thr Ala Ala Ser Ser Glu Met Asp Glu Glu His Gly Gln
 530 535 540
 Leu Asn Val Ser Ser Ser Ala Ala Val Asp Gly Val Ile Ile Ser Leu
 545 550 555 560
 Cys Cys Asn Ser Lys Thr Lys Ser Val Val Leu Gln Leu Ala Asp Gly
 565 570 575
 Gln Ile Phe Lys Tyr Leu Trp Glu Ser Pro Ser Leu Ala Ile Lys Pro
 580 585 590
 Trp Lys Asn Ser Gly Gly Phe Pro Val Arg Phe Pro Tyr Pro Cys Thr
 595 600 605

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Gln Thr Glu Leu Ala Met Ile Gly Glu Glu Glu Cys Val Leu Gly Leu
610 615 620

Thr Asp Arg Cys Arg Phe Phe Ile Asn Asp Ile Glu Val Ala Ser Asn
625 630 635 640

Ile Thr Ser Phe Ala Val Tyr Asp Glu Phe Leu Leu Leu Thr Thr His
645 650 655

Ser His Thr Cys Gln Cys Phe Cys Leu Arg Asp Ala Ser Phe Lys Thr
660 665 670

Leu Gln Ala Gly Leu Ser Ser Asn His Val Ser His Gly Glu Val Leu
675 680 685

Arg Lys Val Glu Arg Gly Ser Arg Ile Val Thr Val Val Pro Gln Asp
690 695 700

Thr Lys Leu Val Leu Gln Met Pro Arg Gly Asn Leu Glu Val Val His
705 710 715 720

His Arg Ala Leu Val Leu Ala Gln Ile Arg Lys Trp Leu Asp Lys Leu
725 730 735

Met Phe Lys Glu Ala Phe Glu Cys Met Arg Lys Leu Arg Ile Asn Leu
740 745 750

Asn Leu Ile Tyr Asp His Asn Pro Lys Val Phe Leu Gly Asn Val Glu
755 760 765

Thr Phe Ile Lys Gln Ile Asp Ser Val Asn His Ile Asn Leu Phe Phe
770 775 780

Thr Glu Leu Lys Glu Glu Asp Val Thr Lys Thr Met Tyr Pro Ala Pro
785 790 795 800

Val Thr Ser Ser Val Tyr Leu Ser Arg Asp Pro Asp Gly Asn Lys Ile
805 810 815

Asp Leu Val Cys Asp Ala Met Arg Ala Val Met Glu Ser Ile Asn Pro
820 825 830

His Lys Tyr Cys Leu Ser Ile Leu Thr Ser His Val Lys Lys Thr Thr
835 840 845

Pro Glu Leu Glu Ile Val Leu Gln Lys Val His Glu Leu Gln Gly Asn
850 855 860

Ala Pro Ser Asp Pro Asp Ala Val Ser Ala Glu Glu Ala Leu Lys Tyr
865 870 875 880

Leu Leu His Leu Val Asp Val Asn Glu Leu Tyr Asp His Ser Leu Gly
885 890 895

Thr Tyr Asp Phe Asp Leu Val Leu Met Val Ala Glu Lys Ser Gln Lys
900 905 910

Asp Pro Lys Glu Tyr Leu Pro Phe Leu Asn Thr Leu Lys Lys Met Glu
915 920 925

Thr Asn Tyr Gln Arg Phe Thr Ile Asp Lys Tyr Leu Lys Arg Tyr Glu
930 935 940

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Lys Ala Ile Gly His Leu Ser Lys Cys Gly Pro Glu Tyr Phe Pro Glu
 945 950 955 960
 Cys Leu Asn Leu Ile Lys Asp Lys Asn Leu Tyr Asn Glu Ala Leu Lys
 965 970 975
 Leu Tyr Ser Pro Ser Ser Gln Gln Tyr Gln Asp Ile Ser Ile Ala Tyr
 980 985 990
 Gly Glu His Leu Met Gln Glu His Met Tyr Glu Pro Ala Gly Leu Met
 995 1000 1005
 Phe Ala Arg Cys Gly Ala His Glu Lys Ala Leu Ser Ala Phe Leu Thr
 1010 1015 1020
 Cys Gly Asn Trp Lys Gln Ala Leu Cys Val Ala Ala Gln Leu Asn Phe
 1025 1030 1035 1040
 Thr Lys Asp Gln Leu Val Gly Leu Gly Arg Thr Leu Ala Gly Lys Leu
 1045 1050 1055
 Val Glu Gln Arg Lys His Ile Asp Ala Ala Met Val Leu Glu Glu Ser
 1060 1065 1070
 Ala Gln Asp Tyr Glu Glu Ala Val Leu Leu Leu Leu Glu Gly Ala Ala
 1075 1080 1085
 Trp Glu Glu Ala Leu Arg Leu Val Tyr Lys Tyr Asn Arg Leu Asp Ile
 1090 1095 1100
 Ile Glu Thr Asn Val Lys Pro Ser Ile Leu Glu Ala Gln Lys Asn Tyr
 1105 1110 1115 1120
 Met Ala Phe Leu Asp Ser Gln Thr Ala Thr Phe Ser Arg His Lys Lys
 1125 1130 1135
 Arg Leu Leu Val Val Arg Glu Leu Lys Glu Gln Ala Gln Gln Ala Gly
 1140 1145 1150
 Leu Asp Asp Glu Val Pro His Gly Gln Glu Ser Asp Leu Phe Ser Glu
 1155 1160 1165
 Thr Ser Ser Val Val Ser Gly Ser Glu Met Ser Gly Lys Tyr Ser His
 1170 1175 1180
 Ser Asn Ser Arg Ile Ser Ala Arg Ser Ser Lys Asn Arg Arg Lys Ala
 1185 1190 1195 1200
 Glu Arg Lys Lys His Ser Leu Lys Glu Gly Ser Pro Leu Glu Asp Leu
 1205 1210 1215
 Ala Leu Leu Glu Ala Leu Ser Glu Val Val Gln Asn Thr Glu Asn Leu
 1220 1225 1230
 Lys Asp Glu Val Tyr His Ile Leu Lys Val Leu Phe Leu Phe Glu Phe
 1235 1240 1245
 Asp Glu Gln Gly Arg Glu Leu Gln Lys Ala Phe Glu Asp Thr Leu Gln
 1250 1255 1260
 Leu Met Glu Arg Ser Leu Pro Glu Ile Trp Thr Leu Thr Tyr Gln Gln

1265 1270 1275 1280
Asn Ser Ala Thr Pro Val Leu Gly Pro Asn Ser Thr Ala Asn Ser Ile
1285 1290 1295
Met Ala Ser Tyr Gln Gln Gln Lys Thr Ser Val Pro Val Leu Asp Ala
1300 1305 1310
Glu Leu Phe Ile Pro Pro Lys Ile Asn Arg Arg Thr Gln Trp Lys Leu
1315 1320 1325
Ser Leu Leu Asp
1330

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<210> 6
<211> 1213
<212> PRT
<213> Drosophila melanogaster
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<400> 6
Met Arg Asn Leu Lys 5 Leu Arg Tyr Cys Lys 10 Glu Leu Asn Ala Val 15 Ala
His Pro Gln His 20 Leu Leu Leu Gln Pro 25 Glu Leu Asn Gly Gly 30 Ala Ser
Asp Ile Tyr 35 Phe Val Val Ala Asp 40 Asn Lys Thr Tyr Ala 45 Val Gln Glu
Ser Gly 50 Asp Val Arg Leu Lys 55 Val Ile Ala Asp Leu 60 Pro Asp Ile Val
Gly 65 Val Glu Phe Leu Gln 70 Leu Asp Asn Ala Ile 75 Cys Val Ala Ser Gly 80
Ala Gly Glu Val Ile 85 Leu Val Asp Pro Gln 90 Thr Gly Ala Thr Ser 95 Glu
Gly Thr Phe Cys 100 Asp Val Gly Ile Glu 105 Ser Met Ala Trp Ser 110 Pro Asn
Gln Glu Val 115 Val Ala Phe Val Thr 120 Arg Thr His Asn Val 125 Val Leu Met
Thr Ser Thr Phe Asp Val Ile 135 Ala Glu Gln Pro Leu 140 Asp Ala Glu Leu
Asp 145 Pro Asp Gln Gln Phe 150 Val Asn Val Gly Trp 155 Gly Lys Lys Glu Thr 160
Gln Phe His Gly Ser 165 Glu Gly Lys Gln Ala 170 Ala Lys Gln Lys Glu Ser
Asp Ser Thr Phe 180 Thr Arg Asp Glu Gln 185 Glu Leu Asn Gln Asp 190 Val Ser
Ile Ser Trp Arg Gly Asp Gly Glu 200 Phe Phe Val Val Ser 205 Tyr Val Ala
Ala Gln Leu Gly Arg Thr Phe 215 Lys Val Tyr Asp Ser 220 Glu Gly Lys Leu

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Asn His Thr Ala Glu Lys Ser Ala Asn Leu Lys Asp Ser Val Val Trp
 225 230 235 240
 Arg Pro Thr Gly Asn Trp Ile Ala Val Pro Gln Gln Phe Pro Asn Lys
 245 250 255
 Ser Thr Ile Ala Leu Phe Glu Lys Asn Gly Leu Arg His Arg Glu Leu
 260 265 270
 Val Leu Pro Phe Asp Leu Gln Glu Glu Pro Val Val Gln Leu Arg Trp
 275 280 285
 Ser Glu Asp Ser Asp Ile Leu Ala Ile Arg Thr Cys Ala Lys Glu Glu
 290 295 300
 Gln Arg Val Tyr Leu Tyr Thr Ile Gly Asn Tyr His Trp Tyr Leu Lys
 305 310 315 320
 Gln Val Leu Ile Phe Glu Gln Ala Asp Pro Leu Ala Leu Leu His Trp
 325 330 335
 Asp Thr Arg Cys Gly Ala Glu His Thr Leu His Val Leu Lys Glu Ser
 340 345 350
 Gly Lys His Leu Val Tyr Arg Trp Ala Phe Ala Val Asp Arg Asn Asn
 355 360 365
 Ser Ile Val Gly Val Ile Asp Gly Lys Arg Leu Leu Leu Thr Asp Phe
 370 375 380
 Asp Glu Ala Ile Val Pro Pro Pro Met Ser Lys Glu Leu Gln Lys Pro
 385 390 395 400
 Ile Met Leu Met Pro Asp Ala Glu Leu Ser Gly Leu His Leu Ala Asn
 405 410 415
 Leu Thr His Phe Ser Pro His Tyr Leu Leu Ala Thr His Ser Ser Ala
 420 425 430
 Gly Ser Thr Arg Leu Leu Leu Leu Ser Tyr Lys Asp Asn Asp Asn Lys
 435 440 445
 Pro Gly Glu Trp Phe Tyr Arg Val His Ser Ser Val Arg Ile Asn Gly
 450 455 460
 Leu Val Asn Ala Val Ala Val Ala Pro Tyr Ala Met Asn Glu Phe Tyr
 465 470 475 480
 Val Gln Thr Val Asn Asn Gly His Thr Tyr Glu Val Ser Leu Lys Ala
 485 490 495
 Asp Lys Thr Leu Lys Val Glu Arg Ser Tyr Val Gln Leu His Glu Pro
 500 505 510
 Ala Asp Gln Ile Asp Trp Val Ile Val Lys Gly Cys Ile Trp Asp Gly
 515 520 525
 Tyr Thr Gly Ala Leu Val Thr Leu Arg Asn Gln His Leu Leu His Ile
 530 535 540
 Asp Gly Tyr Arg Ile Gly Glu Asp Val Thr Ser Phe Cys Val Val Thr
 545 550 555 560

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Asn Tyr Leu Val Tyr Thr Gln Leu Asn Ala Met His Phe Val Gln Leu
 565 570 575
 Asp Asp Arg Arg Gln Val Ala Ser Arg Asn Ile Glu Arg Gly Ala Lys
 580 585 590
 Ile Val Thr Ala Val Ala Arg Lys Ala Arg Val Val Leu Gln Leu Pro
 595 600 605
 Arg Gly Asn Leu Glu Ala Ile Cys Pro Arg Val Leu Val Leu Glu Leu
 610 615 620
 Val Gly Asp Leu Leu Glu Arg Gly Lys Tyr Gln Lys Ala Ile Glu Met
 625 630 635 640
 Ser Arg Lys Gln Arg Ile Asn Leu Asn Ile Ile Phe Asp His Asp Val
 645 650 655
 Lys Arg Phe Val Ser Ser Val Gly Ala Phe Leu Asn Asp Ile Asn Glu
 660 665 670
 Pro Gln Trp Leu Cys Leu Phe Leu Ser Glu Leu Gln Asn Glu Asp Phe
 675 680 685
 Thr Lys Gly Met Tyr Ser Ser Asn Tyr Asp Ala Ser Lys Gln Thr Tyr
 690 695 700
 Pro Ser Asp Tyr Arg Val Asp Gln Lys Val Phe Tyr Val Cys Arg Leu
 705 710 715 720
 Leu Glu Gln Gln Met Asn Arg Phe Val Ser Arg Phe Arg Leu Pro Leu
 725 730 735
 Ile Thr Ala Tyr Val Lys Leu Gly Cys Leu Glu Met Ala Leu Gln Val
 740 745 750
 Ile Trp Lys Glu Gln Gln Glu Asp Ala Ser Leu Ala Asp Gln Leu Leu
 755 760 765
 Gln His Leu Leu Tyr Leu Val Asp Val Asn Asp Leu Tyr Asn Val Ala
 770 775 780
 Leu Gly Thr Tyr Asp Phe Gly Leu Val Leu Phe Val Ala Gln Lys Ser
 785 790 795 800
 Gln Lys Asp Pro Lys Glu Phe Leu Pro Tyr Leu Asn Asp Leu Lys Ala
 805 810 815
 Leu Pro Ile Asp Tyr Arg Lys Phe Arg Ile Asp Asp His Leu Lys Arg
 820 825 830
 Tyr Thr Ser Ala Leu Ser His Leu Ala Ala Cys Gly Glu Gln His Tyr
 835 840 845
 Glu Glu Ala Leu Glu Tyr Ile Arg Lys His Gly Leu Tyr Thr Asp Gly
 850 855 860
 Leu Ala Phe Tyr Arg Glu His Ile Glu Phe Gln Lys Asn Ile Tyr Val
 865 870 875 880

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Ala Tyr Ala Asp His Leu Arg Ala Ile Ala Lys Leu Asp Asn Ala Ser
885 890 895

Leu Met Tyr Glu Arg Gly Gly Gln Leu Gln Gln Ala Leu Leu Ser Ala
900 905 910

Lys His Thr Leu Asp Trp Gln Arg Val Leu Val Leu Ala Lys Lys Leu
915 920 925

Ser Glu Pro Leu Asp Gln Val Ala Gln Ser Leu Val Gly Pro Leu Gln
930 935 940

Gln Gln Gly Arg His Met Glu Ala Tyr Glu Leu Val Lys Glu His Cys
945 950 955 960

Gln Asp Arg Lys Arg Gln Phe Asp Val Leu Leu Glu Gly His Leu Tyr
965 970 975

Ser Arg Ala Ile Tyr Glu Ala Gly Leu Glu Asp Asp Asp Val Ser Glu
980 985 990

Lys Ile Ala Pro Ala Leu Leu Ala Tyr Gly Val Gln Leu Glu Ser Ser
995 1000 1005

Leu Gln Ala Asp Leu Gln Leu Phe Leu Asp Tyr Lys Gln Arg Leu Leu
1010 1015 1020

Asp Ile Arg Arg Asn Gln Ala Lys Ser Gly Glu Gly Tyr Ile Asp Thr
1025 1030 1035 1040

Asp Val Asn Leu Lys Glu Val Asp Leu Leu Ser Asp Thr Thr Ser Leu
1045 1050 1055

His Ser Ser Gln Tyr Ser Gly Thr Ser Arg Arg Thr Gly Lys Thr Phe
1060 1065 1070

Arg Ser Ser Lys Asn Arg Arg Lys His Glu Arg Lys Leu Phe Ser Leu
1075 1080 1085

Lys Pro Gly Asn Pro Phe Glu Asp Ile Ala Leu Ile Asp Ala Leu His
1090 1095 1100

Asn His Val Thr Lys Ile Ala Gln Gln Gln Gln Pro Val Arg Asp Thr
1105 1110 1115 1120

Cys Lys Ala Leu Leu Gln Leu Ala Asn Ala Ala Asp Ala Asp Pro Leu
1125 1130 1135

Ala Ala Ala Leu Gln Arg Glu Phe Lys Thr Leu Leu Gln Ala Val Asp
1140 1145 1150

Ala Ala Leu Asp Glu Ile Trp Thr Pro Glu Leu Arg Gly Asn Gly Leu
1155 1160 1165

Met Ala Asp His Leu Thr Gly Pro Asn Val Asp Tyr Leu Ala Leu Gln
1170 1175 1180

Lys Glu Gln Arg Tyr Ala Leu Leu Ser Pro Leu Lys Arg Phe Lys Pro
1185 1190 1195 1200

Gln Leu Ile Met Met Asp Trp Gln His Glu Ile Leu Gln
1205 1210

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

<210> 7

<211> 1349

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 7

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Met Val Glu His Asp Lys Ser Gly Ser Lys Arg Gln Glu Leu Arg Ser
 1          5          10          15
Asn Met Arg Asn Leu Ile Thr Leu Asn Lys Gly Lys Phe Lys Pro Thr
 20          25          30
Ala Ser Thr Ala Glu Gly Asp Glu Asp Asp Leu Ser Phe Thr Leu Leu
 35          40          45
Asp Ser Val Phe Asp Thr Leu Ser Asp Ser Ile Thr Cys Val Leu Gly
 50          55          60
Ser Thr Asp Ile Gly Ala Ile Glu Val Gln Gln Phe Met Lys Asp Gly
 65          70          75          80
Ser Arg Asn Val Leu Ala Ser Phe Asn Ile Gln Thr Phe Asp Asp Lys
 85          90          95
Leu Leu Ser Phe Val His Phe Ala Asp Ile Asn Gln Leu Val Phe Val
100          105          110
Phe Glu Gln Gly Asp Ile Ile Thr Ala Thr Tyr Asp Pro Val Ser Leu
115          120          125
Asp Pro Ala Glu Thr Leu Ile Glu Ile Met Gly Thr Ile Asp Asn Gly
130          135          140
Ile Ala Ala Ala Gln Trp Ser Tyr Asp Glu Glu Thr Leu Ala Met Val
145          150          155          160
Thr Lys Asp Arg Asn Val Val Val Leu Ser Lys Leu Phe Glu Pro Ile
165          170          175
Ser Glu Tyr His Leu Glu Val Asp Asp Leu Lys Ile Ser Lys His Val
180          185          190
Thr Val Gly Trp Gly Lys Lys Glu Thr Gln Phe Arg Gly Lys Gly Ala
195          200          205
Arg Ala Met Glu Arg Glu Ala Leu Ala Ser Leu Lys Ala Ser Gly Leu
210          215          220
Val Gly Asn Gln Leu Arg Asp Pro Thr Met Pro Tyr Met Val Asp Thr
225          230          235          240
Gly Asp Val Thr Ala Leu Asp Ser His Glu Ile Thr Ile Ser Trp Arg
245          250          255
Gly Asp Cys Asp Tyr Phe Ala Val Ser Ser Val Glu Glu Val Pro Asp
260          265          270
Glu Asp Asp Glu Thr Lys Ser Ile Lys Arg Arg Ala Phe Arg Val Phe
275          280          285
Ser Arg Glu Gly Gln Leu Asp Ser Ala Ser Glu Pro Val Thr Gly Met

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REVSecond Substitute Sequence Listing 1829-4004US1.TXT

290
 295
 300
 Glu His Gln Leu Ser Trp Lys Pro Gln Gly Ser Leu Ile Ala Ser Ile
 305 310 315 320
 Gln Arg Lys Thr Asp Leu Gly Glu Glu Asp Ser Val Asp Val Ile Phe
 325 330 335
 Phe Glu Arg Asn Gly Leu Arg His Gly Glu Phe Asp Thr Arg Leu Pro
 340 345 350
 Leu Asp Glu Lys Val Glu Ser Val Cys Trp Asn Ser Asn Ser Glu Ala
 355 360 365
 Leu Ala Val Val Leu Ala Asn Arg Ile Gln Leu Trp Thr Ser Lys Asn
 370 375 380
 Tyr His Trp Tyr Leu Lys Gln Glu Leu Tyr Ala Ser Asp Ile Ser Tyr
 385 390 395 400
 Val Lys Trp His Pro Glu Lys Asp Phe Thr Leu Met Phe Ser Asp Ala
 405 410 415
 Gly Phe Ile Asn Ile Val Asp Phe Ala Tyr Lys Met Ala Gln Gly Pro
 420 425 430
 Thr Leu Glu Pro Phe Asp Asn Gly Thr Ser Leu Val Val Asp Gly Arg
 435 440 445
 Thr Val Asn Ile Thr Pro Leu Ala Leu Ala Asn Val Pro Pro Pro Met
 450 455 460
 Tyr Tyr Arg Asp Phe Glu Thr Pro Gly Asn Val Leu Asp Val Ala Cys
 465 470 475 480
 Ser Phe Ser Asn Glu Ile Tyr Ala Ala Ile Asn Lys Asp Val Leu Ile
 485 490 495
 Phe Ala Ala Val Pro Ser Ile Glu Glu Met Lys Lys Gly Lys His Pro
 500 505 510
 Ser Ile Val Cys Glu Phe Pro Lys Ser Glu Phe Thr Ser Glu Val Asp
 515 520 525
 Ser Leu Arg Gln Val Ala Phe Ile Asn Asp Ser Ile Val Gly Val Leu
 530 535 540
 Leu Asp Thr Asp Asn Leu Ser Arg Ile Ala Leu Leu Asp Ile Gln Asp
 545 550 555 560
 Ile Thr Gln Pro Thr Leu Ile Thr Ile Val Glu Val Tyr Asp Lys Ile
 565 570 575
 Val Leu Leu Ser Ser Asp Phe Asp Tyr Asn His Leu Val Tyr Glu Thr
 580 585 590
 Arg Asp Gly Thr Val Cys Gln Leu Asp Ala Glu Gly Gln Leu Met Glu
 595 600 605
 Ile Thr Lys Phe Pro Gln Leu Val Arg Asp Phe Arg Val Lys Arg Val
 610 615 620

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

His 625 Asn Thr Ser Ala 630 Glu Asp Asp Asp Asn 635 Trp Ser Ala Glu Ser Ser 640
 Glu Leu Val Ala 645 Phe Gly Ile Thr Asn 650 Asn Gly Lys Leu Phe Ala Asn 655
 Gln Val Leu 660 Ala Ser Ala Val Thr 665 Ser Leu Glu Ile Thr 670 Asp Ser
 Phe Leu 675 Leu Phe Thr Thr Ala Gln 680 His Asn Leu Gln Phe Val His Leu 685
 Asn Ser 690 Thr Asp Phe Lys Pro 695 Leu Pro Leu Val Glu 700 Glu Gly Val Glu
 Asp 705 Glu Arg Val Arg Ala 710 Ile Glu Arg Gly Ser 715 Ile Leu Val Ser Val 720
 Ile Pro Ser Lys 725 Arg Ser Val Val Leu Gln 730 Ala Thr Arg Gly Asn 735 Leu
 Glu Thr Ile Tyr 740 Pro Arg Ile Met Val 745 Leu Ala Glu Val Arg 750 Lys Asn
 Ile Met Ala 755 Lys Arg Tyr Lys Glu 760 Ala Phe Ile Val Cys 765 Arg Thr His
 Arg Ile 770 Asn Leu Asp Ile Leu 775 His Asp Tyr Ala Pro 780 Glu Leu Phe Ile
 Glu 785 Asn Leu Glu Val Phe 790 Ile Asn Gln Ile Gly 795 Arg Val Asp Tyr Leu 800
 Asn Leu Phe Ile 805 Ser Cys Leu Ser Glu 810 Asp Asp Val Thr Lys Thr 815 Lys
 Tyr Lys Glu Thr 820 Leu Tyr Ser Gly Ile 825 Ser Lys Ser Phe Gly 830 Met Glu
 Pro Ala Pro 835 Leu Thr Glu Met Gln 840 Ile Tyr Met Lys Lys 845 Lys Met Phe
 Asp Pro 850 Lys Thr Ser Lys Val 855 Asn Lys Ile Cys Asp 860 Ala Val Leu Asn
 Val 865 Leu Leu Ser Asn Pro 870 Glu Tyr Lys Lys Lys Tyr Leu Gln Thr Ile 880
 Ile Thr Ala Tyr 885 Ala Ser Gln Asn Pro Gln 890 Asn Leu Ser Ala Ala Leu 895
 Lys Leu Ile Ser 900 Glu Leu Glu Asn Ser 905 Glu Glu Lys Asp Ser 910 Cys Val
 Thr Tyr Leu 915 Cys Phe Leu Gln Asp Val 920 Asn Val Val Tyr 925 Lys Ser Ala
 Leu Ser 930 Leu Tyr Asp Val Ser 935 Leu Ala Leu Leu Val 940 Ala Gln Lys Ser
 Gln 945 Met Asp Pro Arg Glu 950 Tyr Leu Pro Phe Leu 955 Gln Glu Leu Gln Asp 960

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Asn Glu Pro Leu Arg Arg Lys Phe Leu Ile Asp Asp Tyr Leu Gly Asn
 965 970 975
 Tyr Glu Lys Ala Leu Glu His Leu Ser Glu Ile Asp Lys Asp Gly Asn
 980 985 990
 Val Ser Glu Glu Val Ile Asp Tyr Val Glu Ser His Asp Leu Tyr Lys
 995 1000 1005
 His Gly Leu Ala Leu Tyr Arg Tyr Asp Ser Glu Lys Gln Asn Val Ile
 1010 1015 1020
 Tyr Asn Ile Tyr Ala Lys His Leu Ser Ser Asn Gln Met Tyr Thr Asp
 1025 1030 1035 1040
 Ala Ala Val Ala Tyr Glu Met Leu Gly Lys Leu Lys Glu Ala Met Gly
 1045 1050 1055
 Ala Tyr Gln Ser Ala Lys Arg Trp Arg Glu Ala Met Ser Ile Ala Val
 1060 1065 1070
 Gln Lys Phe Pro Glu Glu Val Glu Ser Val Ala Glu Glu Leu Ile Ser
 1075 1080 1085
 Ser Leu Thr Phe Glu His Arg Tyr Val Asp Ala Ala Asp Ile Gln Leu
 1090 1095 1100
 Glu Tyr Leu Asp Asn Val Lys Glu Ala Val Ala Leu Tyr Cys Lys Ala
 1105 1110 1115 1120
 Tyr Arg Tyr Asp Ile Ala Ser Leu Val Ala Ile Lys Ala Lys Lys Asp
 1125 1130 1135
 Glu Leu Leu Glu Glu Val Val Asp Pro Gly Leu Gly Glu Gly Phe Gly
 1140 1145 1150

 Ile Ile Ala Glu Leu Leu Ala Asp Cys Lys Gly Gln Ile Asn Ser Gln
 1155 1160 1165
 Leu Arg Arg Leu Arg Glu Leu Arg Ala Lys Lys Glu Glu Asn Pro Tyr
 1170 1175 1180
 Ala Phe Tyr Gly Gln Glu Thr Glu Gln Ala Asp Asp Val Ser Val Ala
 1185 1190 1195 1200
 Pro Ser Glu Thr Ser Thr Gln Glu Ser Phe Phe Thr Arg Tyr Thr Gly
 1205 1210 1215
 Lys Thr Gly Gly Thr Ala Lys Thr Gly Ala Ser Arg Arg Thr Ala Lys
 1220 1225 1230
 Asn Lys Arg Arg Glu Glu Arg Lys Arg Ala Arg Gly Lys Lys Gly Thr
 1235 1240 1245
 Ile Tyr Glu Glu Glu Tyr Leu Val Gln Ser Val Gly Arg Leu Ile Glu
 1250 1255 1260
 Arg Leu Asn Gln Thr Lys Pro Asp Ala Val Arg Val Val Glu Gly Leu
 1265 1270 1275 1280
 Cys Arg Arg Asn Met Arg Glu Gln Ala His Gln Ile Gln Lys Asn Phe

Val Glu Val Leu Asp Leu Leu Lys Ala Asn Val Lys Glu Ile Tyr Ser
1300 1305 1310
Ile Ser Glu Lys Asp Arg Glu Arg Val Asn Glu Asn Gly Glu Val Tyr
1315 1320 1325
Tyr Ile Pro Glu Ile Pro Val Pro Glu Ile His Asp Phe Pro Lys Ser
1330 1335 1340
His Ile Val Asp Phe
1345

<210> 8
<211> 1319
<212> PRT
<213> Arabidopsis thaliana

<400> 8
Met Lys Asn Leu Lys Leu Phe Ser Glu Val Pro Gln Asn Ile Gln Leu
1 5 10 15
His Ser Thr Glu Glu Val Val Gln Phe Ala Ala Thr Asp Ile Asp Gln
20 25 30
Ser Arg Leu Phe Phe Ala Ser Ser Ala Asn Phe Val Tyr Ala Leu Gln
35 40 45
Leu Ser Ser Phe Gln Asn Glu Ser Ala Gly Ala Lys Ser Ala Met Pro
50 55 60
Val Glu Val Cys Ser Ile Asp Ile Glu Pro Gly Asp Phe Ile Thr Ala
65 70 75 80
Phe Asp Tyr Leu Ala Glu Lys Glu Ser Leu Leu Ile Gly Thr Ser His
85 90 95
Gly Leu Leu Leu Val His Asn Val Glu Ser Asp Val Thr Glu Leu Val
100 105 110
Gly Asn Ile Glu Gly Gly Val Lys Cys Ile Ser Pro Asn Pro Thr Gly
115 120 125
Asp Leu Leu Gly Leu Ile Thr Gly Leu Gly Gln Leu Ile Val Met Thr
130 135 140
Tyr Asp Trp Ala Leu Met Tyr Glu Lys Ala Leu Gly Glu Val Pro Glu
145 150 155 160
Gly Gly Tyr Val Arg Glu Thr Asn Asp Leu Ser Val Asn Cys Gly Gly
165 170 175
Ile Ser Ile Ser Trp Arg Gly Asp Gly Lys Tyr Phe Ala Thr Met Gly
180 185 190
Glu Val Tyr Glu Ser Gly Cys Met Ser Lys Lys Ile Lys Ile Trp Glu
195 200 205
Ser Asp Ser Gly Ala Leu Gln Ser Ser Ser Glu Thr Lys Glu Phe Thr
210 215 220

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Gln Gly Ile Leu Glu Trp Met Pro Ser Gly Ala Lys Ile Ala Ala Val
 225 230 235 240
 Tyr Lys Arg Lys Ser Asp Asp Ser Ser Pro Ser Ile Ala Phe Phe Glu
 245 250 255
 Arg Asn Gly Leu Glu Arg Ser Ser Phe Arg Ile Gly Glu Pro Glu Asp
 260 265 270
 Ala Thr Glu Ser Cys Glu Asn Leu Lys Trp Asn Ser Ala Ser Asp Leu
 275 280 285
 Leu Ala Gly Val Val Ser Cys Lys Thr Tyr Asp Ala Ile Arg Val Trp
 290 295 300
 Phe Phe Ser Asn Asn His Trp Tyr Leu Lys Gln Glu Ile Arg Tyr Pro
 305 310 315 320
 Arg Glu Ala Gly Val Thr Val Met Trp Asp Pro Thr Lys Pro Leu Gln
 325 330 335
 Leu Ile Cys Trp Thr Leu Ser Gly Gln Val Ser Val Arg His Phe Met
 340 345 350
 Trp Val Thr Ala Val Met Glu Asp Ser Thr Ala Phe Val Ile Asp Asn
 355 360 365
 Ser Lys Ile Leu Val Thr Pro Leu Ser Leu Ser Leu Met Pro Pro Pro
 370 375 380
 Met Tyr Leu Phe Ser Leu Ser Phe Ser Ser Ala Val Arg Asp Ile Ala
 385 390 395 400
 Tyr Tyr Ser Arg Asn Ser Lys Asn Cys Leu Ala Val Phe Leu Ser Asp
 405 410 415
 Gly Asn Leu Ser Phe Val Glu Phe Pro Ala Pro Asn Thr Trp Glu Asp
 420 425 430
 Leu Glu Gly Lys Asp Phe Ser Val Glu Ile Ser Asp Cys Lys Thr Ala
 435 440 445
 Leu Gly Ser Phe Val His Leu Leu Trp Leu Asp Val His Ser Leu Leu
 450 455 460
 Cys Val Ser Ala Tyr Gly Ser Ser His Asn Lys Cys Leu Ser Ser Gly
 465 470 475 480
 Gly Tyr Asp Thr Glu Leu His Gly Ser Tyr Leu Gln Glu Val Glu Val
 485 490 495
 Val Cys His Glu Asp His Val Pro Asp Gln Val Thr Cys Ser Gly Phe
 500 505 510
 Lys Ala Ser Ile Thr Phe Gln Thr Leu Leu Glu Ser Pro Val Leu Ala
 515 520 525
 Leu Ala Trp Asn Pro Ser Lys Arg Asp Ser Ala Phe Val Glu Phe Glu
 530 535 540
 Gly Gly Lys Val Leu Gly Tyr Ala Ser Arg Ser Glu Ile Met Glu Thr
 545 550 555 560

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Arg Ser Ser Asp Asp Ser Val Cys Phe Pro Ser Thr Cys Pro Trp Val
565 570 575

Arg Val Ala Gln Val Asp Ala Ser Gly Val His Lys Pro Leu Ile Cys
580 585 590

Gly Leu Asp Asp Met Gly Arg Leu Ser Ile Asn Gly Lys Asn Leu Cys
595 600 605

Asn Asn Cys Ser Ser Phe Ser Phe Tyr Ser Glu Leu Ala Asn Glu Val
610 615 620

Val Thr His Leu Ile Ile Leu Thr Lys Gln Asp Phe Leu Phe Ile Val
625 630 635 640

Asp Thr Lys Asp Val Leu Asn Gly Asp Val Ala Leu Gly Asn Val Phe
645 650 655

Phe Val Ile Asp Gly Arg Arg Arg Asp Glu Glu Asn Met Ser Tyr Val
660 665 670

Asn Ile Trp Glu Arg Gly Ala Lys Val Ile Gly Val Leu Asn Gly Asp
675 680 685

Glu Ala Ala Val Ile Leu Gln Thr Met Arg Gly Asn Leu Glu Cys Ile
690 695 700

Tyr Pro Arg Lys Leu Val Leu Ser Ser Ile Thr Asn Ala Leu Ala Gln
705 710 715 720

Gln Arg Phe Lys Asp Ala Phe Asn Leu Val Arg Arg His Arg Ile Asp
725 730 735

Phe Asn Val Ile Val Asp Leu Tyr Gly Trp Gln Ala Phe Leu Gln Ser
740 745 750

Ala Val Ala Phe Val Glu Gln Val Asn Asn Leu Asn His Val Thr Glu
755 760 765

Phe Val Cys Ala Met Lys Asn Glu Asp Val Thr Glu Thr Leu Tyr Lys
770 775 780

Lys Phe Ser Phe Ser Lys Lys Gly Asp Glu Val Phe Arg Val Lys Asp
785 790 795 800

Ser Cys Ser Asn Lys Val Ser Ser Val Leu Gln Ala Ile Arg Lys Ala
805 810 815

Leu Glu Glu His Ile Pro Glu Ser Pro Ser Arg Glu Leu Cys Ile Leu
820 825 830

Thr Thr Leu Ala Arg Ser Asp Pro Pro Ala Ile Glu Glu Ser Leu Leu
835 840 845

Arg Ile Lys Ser Val Arg Glu Met Glu Leu Leu Asn Ser Ser Asp Asp
850 855 860

Ile Arg Lys Lys Ser Cys Pro Ser Ala Glu Glu Ala Leu Lys His Leu
865 870 875 880

Leu Trp Leu Leu Asp Ser Glu Ala Val Phe Glu Ala Ala Leu Gly Leu

REVSecond Substitute Sequence Listing 1829-4004US1.TXT
885 890 895

Tyr Asp Leu Asn Leu Ala Ala Ile Val Ala Leu Asn Ser Gln Arg Asp
900 905 910

Pro Lys Glu Phe Leu Pro Tyr Leu Gln Glu Leu Glu Lys Met Pro Glu
915 920 925

Ser Leu Met His Phe Lys Ile Asp Ile Lys Leu Gln Arg Phe Asp Ser
930 935 940

Ala Leu Arg Asn Ile Val Ser Ala Gly Val Gly Tyr Phe Pro Asp Cys
945 950 955 960

Met Asn Leu Ile Lys Lys Asn Pro Gln Leu Phe Pro Leu Gly Leu Leu
965 970 975

Leu Ile Thr Asp Pro Glu Lys Lys Leu Val Val Leu Glu Ala Trp Ala
980 985 990

Asp His Leu Ile Asp Glu Lys Arg Phe Glu Asp Ala Ala Thr Thr Tyr
995 1000 1005

Leu Cys Cys Cys Lys Leu Glu Lys Ala Ser Lys Ala Tyr Arg Glu Cys
1010 1015 1020

Gly Asp Trp Ser Gly Val Leu Arg Val Gly Ala Leu Met Lys Leu Gly
1025 1030 1035 1040

Lys Asp Glu Ile Leu Lys Leu Ala Tyr Glu Leu Cys Glu Glu Val Asn
1045 1050 1055

Ala Leu Gly Lys Pro Ala Glu Ala Ala Lys Ile Ala Leu Glu Tyr Cys
1060 1065 1070

Ser Asp Ile Ser Gly Gly Ile Ser Leu Leu Ile Asn Ala Arg Glu Trp
1075 1080 1085

Glu Glu Ala Leu Arg Val Ala Phe Leu His Thr Ala Asp Asp Arg Ile
1090 1095 1100

Ser Val Val Lys Ser Ser Ala Leu Glu Cys Ala Ser Gly Leu Val Ser
1105 1110 1115 1120

Glu Phe Lys Glu Ser Ile Glu Lys Val Gly Lys Tyr Leu Thr Arg Tyr
1125 1130 1135

Leu Ala Val Arg Gln Arg Arg Leu Leu Ala Ala Lys Leu Lys Ser
1140 1145 1150

Glu Glu Arg Ser Val Val Asp Leu Asp Asp Asp Thr Ala Ser Glu Ala
1155 1160 1165

Ser Ser Asn Leu Ser Gly Met Ser Ala Tyr Thr Leu Gly Thr Arg Arg
1170 1175 1180

Gly Ser Ala Ala Ser Val Ser Ser Ser Asn Ala Thr Ser Arg Ala Arg
1185 1190 1195 1200

Asp Leu Arg Arg Gln Arg Lys Ser Gly Lys Ile Arg Ala Gly Ser Ala
1205 1210 1215

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

Gly Glu Glu Met Ala Leu Val Asp His Leu Lys Gly Met Arg Met Thr
1220 1225 1230

Asp Gly Gly Lys Arg Glu Leu Lys Ser Leu Leu Ile Cys Leu Val Thr
1235 1240 1245

Leu Gly Glu Met Glu Ser Ala Gln Lys Leu Gln Gln Thr Ala Glu Asn
1250 1255 1260

Phe Gln Val Ser Gln Val Ala Ala Val Glu Leu Ala His Asp Thr Val
1265 1270 1275 1280

Ser Ser Glu Ser Val Asp Glu Glu Val Tyr Cys Phe Glu Arg Tyr Ala
1285 1290 1295

Gln Lys Thr Arg Ser Thr Ala Arg Asp Ser Asp Ala Phe Ser Trp Met
1300 1305 1310

Leu Lys Val Phe Ile Ser Pro
1315

<210> 9
<211> 1178
<212> PRT
<213> Caenorhabditis elegans

<400> 9
Met Lys Asn Leu Gln Ile Gly Ser Val Lys Thr Phe Glu Asn Pro Glu
1 5 10 15

Ile Ala Gly Ala Asp Asp Phe Ala Val His Pro Ile Leu Gln Thr Ile
20 25 30

Ala Val Ser Thr Lys Asn Glu Leu Leu Leu Glu Asn Asn Leu Ile
35 40 45

Ser Ser Thr Ile Lys Trp Ala Glu Gln Arg Arg Glu Leu Glu Val Ile
50 55 60

Ser Leu Ser Phe Arg Thr Asp Gly Asn Gln Ile Val Val Ile Leu Ala
65 70 75 80

Asp Gly Arg Ala Leu Ile Val Glu Asp Gly Glu Val Met Asp Leu Glu
85 90 95

Ile Ala Glu Leu Thr Asp Thr Thr Val Ser Ala Ala Glu Trp Thr Ala
100 105 110

Asp Glu Gln Thr Leu Ala Leu Ala Asp Asn Gln Thr Leu Tyr Leu Ala
115 120 125

Asp Ser Ser Leu Val Pro Phe Ala Glu Arg Pro Leu Ile Phe Ser Glu
130 135 140

Asn Glu Arg Lys Ser Ala Pro Val Asn Val Gly Trp Gly Ser Glu Ser
145 150 155 160

Thr Gln Phe Arg Gly Ser Ala Gly Lys Leu Lys Pro Gly Glu Lys Ile
165 170 175

Glu Lys Glu Lys Glu Gln Ile Glu Gln His Ser Arg Lys Thr Ser Val

REVSecond Substitute Sequence Listing 1829-4004US1.TXT
180 185 190

His Trp Arg Trp Asp Gly Glu Ile Val Ala Val Ser Phe Tyr Ser Ser
195 200 205

Gln Asn Asp Thr Arg Asn Leu Thr Val Phe Asp Arg Asn Gly Glu Ile
210 215 220

Leu Asn Asn Met Asn Ile Arg Asn Ile Tyr Leu Ser His Cys Phe Ala
225 230 235 240

His Lys Pro Asn Ala Asn Leu Leu Cys Ser Ala Ile Gln Glu Asn Gly
245 250 255

Ser Asp Asp Arg Ile Val Ile Tyr Glu Arg Asn Gly Glu Thr Arg Asn
260 265 270

Ser Tyr Val Val Lys Trp Pro Ala Asn Gln Ile Glu Asp Arg Arg Ile
275 280 285

Ile Glu Lys Ile Glu Trp Asn Ser Thr Gly Thr Ile Leu Ser Met Gln
290 295 300

Thr Ser Leu Gly Lys Lys His Gln Leu Glu Phe Trp His Leu Ser Asn
305 310 315 320

Tyr Glu Phe Thr Arg Lys Cys Tyr Trp Lys Phe Ser Glu Ser Ile Ile
325 330 335

Trp Lys Trp Ser Thr Val Glu Cys Gln Asn Ile Glu Val Leu Leu Glu
340 345 350

Ser Gly Gln Phe Phe Ser Val His Ile Thr Pro Thr Ala Ser Phe Ser
355 360 365

Asp Val Ile Ser Gln Asn Val Val Val Ala Thr Asp Glu Leu Arg Met
370 375 380

Tyr Ser Leu Cys Arg Arg Val Val Pro Pro Pro Met Cys Asp Tyr Ser
385 390 395 400

Ile Gln Cys Leu Ser Asp Ile Val Ala Tyr Thr Thr Ser Thr His His
405 410 415

Val His Val Ile Thr Ser Asp Trp Lys Ile Ile Ser Cys Met Leu Phe
420 425 430

Phe Lys Lys Lys Lys Arg Asn Tyr Ser Asn Pro Phe Phe Arg Lys Lys
435 440 445

Tyr Ile Leu Glu Ile Leu Lys Val Pro Ser His Lys Thr Tyr Phe Ala
450 455 460

Cys Phe Ala Val Ser Gln Asp Thr Asp Gly Tyr Lys Phe Asn Ser Asp
465 470 475 480

Arg Ala Ser Ile Asp Glu Val Leu His Thr Glu Val Thr Glu Gly Ile
485 490 495

Ile Cys Gly Phe Val Tyr Asp Glu Pro Ser Glu Ser Tyr Ile Ile Trp
500 505 510

Asn Val Ser His Gly Lys His Gln Ile Ser Arg Val Gly Ala Asn Pro

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515

520

525

Glu Lys Ile Phe Glu Gly Glu Asn Ile Gly Trp Ile Gly Val Asn Pro
 530 535 540
 Ser Asn Lys His Val Glu Ile Ala Ser Asn Asp Gly Lys Phe Ile Asp
 545 550 555 560
 Leu Asn Thr Lys Glu Glu Leu Phe Lys Ile Asp Lys Phe Glu Ser Thr
 565 570 575
 Glu Val His Phe Ile Gln Val Cys His Gly Ile Leu Asn His His Val
 580 585 590
 Ile Gln Val Asp Asn Ser Met Leu Phe Leu Asp Ser Glu Arg Val Ser
 595 600 605
 Gln Asp Ala Ile Ser Ile Leu Thr Arg Gly Ser Asp Ile Leu Leu Ile
 610 615 620
 Asp Phe Asp Asn Lys Leu Arg Phe Ile Asp Ala Glu Ser Gly Lys Thr
 625 630 635 640
 Leu Glu Asp Val Arg Asn Val Glu Ala Gly Cys Glu Leu Val Ala Cys
 645 650 655
 Asp Ser Gln Ser Ala Asn Val Ile Leu Gln Ala Ala Arg Gly Asn Leu
 660 665 670
 Glu Thr Ile Gln Pro Arg Arg Tyr Val Met Ala His Thr Arg Asp Leu
 675 680 685
 Leu Asp Arg Lys Glu Tyr Ile Ala Ser Phe Lys Trp Met Lys Lys His
 690 695 700
 Arg Val Asp Met Ser Phe Ala Met Lys Tyr Lys Gly Asp Asp Leu Glu
 705 710 715 720
 Asp Asp Ile Pro Ile Trp Leu Lys Thr Ser Asn Asp Ser Gln Phe Leu
 725 730 735
 Glu Gln Leu Leu Ile Ser Cys Thr Glu Val Phe Glu Asp Ala Gly Ser
 740 745 750
 Ser Leu Cys Met Thr Val Ala Arg Tyr Val Arg Asp Leu Ser Asp Ala
 755 760 765
 Glu Lys Thr Lys Met Phe Pro Leu Leu Leu Thr Ala Leu Leu Ser Ala
 770 775 780
 Arg Ser Lys Pro Ser Lys Val Asn Asp Cys Leu Lys Glu Val Gln Glu
 785 790 795 800
 His Val Glu Lys Ile Ala Asp Arg Lys Asp Val Phe Thr Arg Asn Ser
 805 810 815
 Leu His His Ile Ser Phe Phe Val Pro Ala Lys Glu Leu Phe Asn Cys
 820 825 830
 Ala Leu Ser Thr Tyr Asp Leu Lys Leu Ala Gln Gln Val Ala Glu Ala
 835 840 845

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Ser Asn Tyr Asp Pro Lys Glu Tyr Leu Pro Val Leu Asn Lys Leu Asn
850 855 860

Arg Val Met Cys Thr Leu Glu Arg Gln Tyr Arg Ile Asn Val Val Arg
865 870 875 880

Glu Ala Trp Ile Asp Ala Val Ser Ser Leu Phe Leu Leu Asp Ser Ser
885 890 895

Lys Glu Arg Gly Ser Glu Glu Thr Trp Trp Asn Asp Ile Glu Asp Ile
900 905 910

Ile Ile Gln Arg Glu Lys Leu Tyr Gln Asp Ala Leu Thr Leu Val Lys
915 920 925

Pro Gly Asp Arg Arg Tyr Lys Gln Cys Cys Glu Leu Tyr Ala Glu Leu
930 935 940

Glu Arg Lys Val His Trp Arg Glu Ala Ala Leu Phe Tyr Glu Leu Ser
945 950 955 960

Gly Asn Ser Glu Lys Thr Leu Lys Cys Trp Glu Met Ser Arg Asp Val
965 970 975

Asp Gly Leu Ala Ala Ser Ala Arg Arg Leu Ala Val Asp Ala Gly Lys
980 985 990

Leu Lys Ile His Ala Ile Lys Met Ser Thr Thr Leu Arg Glu Ala Arg
995 1000 1005

Gln Pro Lys Glu Leu Ala Lys Ala Leu Lys Leu Ala Gly Ser Ser Ser
1010 1015 1020

Thr Gln Ile Val His Val Leu Cys Asp Ala Phe Glu Trp Leu Asp Ala
1025 1030 1035 1040

Ser Arg Glu Val Glu Val Gly Lys Glu Glu Ala Leu Lys Lys Ala Ala
1045 1050 1055

Leu Ser Arg Asn Asp Gln Val Leu Met Asp Leu Glu Arg Arg Lys Thr
1060 1065 1070

Glu Phe Glu Asn Tyr Lys Lys Arg Leu Ala Val Val Arg Glu Asn Lys
1075 1080 1085

Leu Lys Arg Val Glu Gln Phe Ala Ala Gly Glu Val Asp Asp Leu Arg
1090 1095 1100

Asp Asp Ile Ser Val Ile Ser Ser Ile Ser Ser Arg Ser Gly Ser Ser
1105 1110 1115 1120

Lys Val Ser Met Ala Ser Thr Val Arg Arg Lys Gln Ile Glu Lys Lys
1125 1130 1135

Lys Ser Ser Leu Lys Glu Gly Gly Glu Tyr Glu Asp Ser Ala Leu Leu
1140 1145 1150

Asn Val Leu Ser Glu Asn Tyr Arg Trp Leu Glu Asn Ile Gly Ser Glu
1155 1160 1165

Phe Cys Phe Pro Trp Asn Phe Asn Ile Leu

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ttttctctga tgcagct 17

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cttgaaaaac tgtaggc 17

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<400> 15
ggtgtctctc ttcagcc 17

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<400> 16

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

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<212> DNA

<213> Mus sp.

<400> 17

aggttctgct ttcagac

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<212> DNA

<213> Mus sp.

<400> 18

ttttgtccct accaggt

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<400> 19

tccctccaca cacagtc

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<212> DNA

<213> Mus sp.

<400> 20

cttttcattg tgtagac

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<210> 21

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<400> 21

ttttttgttt tctaggt

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<210> 22

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<213> Mus sp.

<400> 22

ctaataatttg aacagga

17

<210> 23

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<400> 23

REVSecond Substitute Sequence Listing 1829-4004US1.TXT

ttttttttgc tttagtt

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ttaatcttac aacagag

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<400> 25
ttcatttctt tgcagga

17

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<400> 26
tcttgcctgt tgcaggt

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<400> 27
cactggtatt tttagt

17

<210> 28
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<400> 28
gggttttatt ttgagat

17

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tactttcttt gataggt

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<400> 33
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<210> 35
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ttgctgtcctt ttcagga

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ctcttccctt gtcagga

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attatgcatc ctcagcc

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tgtaatttct gacagga

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ctgttttctg cttagg

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<400> 46
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17

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<400> 47
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17

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<400> 48
 aggtaggtgt aaggcct

17

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17

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tggttaaggcg ggatgat

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17

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 aagtaagttg ctgcaaa

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gggtgaggat cagagtt

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aggtgaatag acacggc

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aggtatgtag gcttggt

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aagtaagctc tcctata

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aggtaagctg actcttc

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aggttaagtat tttgata

17

<210> 68

<211> 17

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<400> 68

aagtgggtgc tgtgtgt

17

<210> 69

<211> 17

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<400> 69

aggtagagac ctgcgcg

17

<210> 70

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<400> 70

aggtatgtgg agttgag

17

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<400> 71

tggttaagggt ttttttt

17

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REVSecond Substitute Sequence Listing 1829-4004US1.TXT

aggatatgtgg tgggtta

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aggtaagcag ggccatt

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<400> 74
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<400> 75
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<400> 77
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17

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<400> 79

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17

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<400> 80

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19

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<223> Description of Artificial Sequence: Primer

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REVSecond Substitute Sequence Listing 1829-4004US1.TXT

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ggttcacsga ttgtc 15

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<400> 87
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